Product Insert

VariantPlex™ Complete Solid Tumor panel

VariantPlex Complete Solid Tumor

Description

The VariantPlex Complete Solid Tumor panel is a balanced pool of gene-specific primer (GSP) oligonucleotides that is optimized for use with VariantPlex reagents and molecular barcode (MBC) adapters to produce targeted NGS libraries. This product insert should be used in conjunction with VariantPlex HS/HGC protocol for Illumina® (RA-DOC-056).

VariantPlex Complete Solid Tumor contains **19,943** GSPs targeting **430** genes commonly mutated in solid tumor cancer types.

Description	Part number	Storage
VariantPlex Complete Solid Tumor GSP1, 8 reactions	SA22534081	–20°C ± 10°C
VariantPlex Complete Solid Tumor GSP2, 8 reactions	SA22534082	
PreSeq™ DNA QC Assay Standard, 32 µL	SA0597	
PreSeq™ DNA QC Assay 10X Primer Mix, 120 µL	SA0598	

Required reagent volumes

Protocol reference	Protocol step	Reagent	Volume per reaction (µL)
A	Ligation Step 2 Elution	5mM NaOH	32
B	First PCR	VariantPlex Complete Solid Tumor GSP1	8
C	First PCR	10mM Tris-HCl pH 8.0	34
D	First PCR	Purified PCR1 eluate	32
E	Second PCR	VariantPlex Complete Solid Tumor GSP2	8

Recommended PCR cycling

	Step	Temperature (°C)	Time	Cycles
First PCR reaction	**1**	95	3 min	1
	2	95	30 sec	15
	3	60	10 min (100% ramp rate)	
	4	72	3 min	1
	5	4	Hold	1
Second PCR reaction	**1**	95	3 min	1
	2	95	30 sec	20†
	3	65	10 min (100% ramp rate)	
	4	72	3 min	1
	5	4	Hold	1

†The number of PCR2 cycles may be decreased if you regularly experience library yields greater than 200 nM.

Recommended reads and multiplexing

VariantPlex Complete Solid Tumor libraries should be sequenced to a minimum of **45M** reads. Starting read depth recommendations for standard profiling may be adjusted based on user needs.

Archer™ Analysis settings

Sequencing data should be processed using Archer Analysis (v7.2, or greater). The VariantPlex Complete Solid Tumor panel is compatible with the ***SNV/Indel, Copy Number Variation, Structural Variation, MSI, and TMB*** pipelines, found under the ***DNA*** Input Type**.** The recommended TMB settings in Archer Analysis are *High Threshold for TMB* = 17.5 and *Low Threshold* for TMB = 6 for VariantPlex Complete Solid Tumor. As with most Analysis settings, these may be adjusted based on user needs. Selection of the DNA Target Coverage pipeline is optional (see the Archer Analysis User Guide for more details on setting up your analysis).

Archer Analysis processing of VariantPlex Complete Solid Tumor libraries requires a one-time upload of the Panel GTF. When performing DNA Target Coverage analysis, users must also select a Region of Interest BED file. Users may optionally add a Targeted Mutations VCF file for targeted SNV/Indel detection. Files can be obtained by contacting archer-tech@idtdna.com

Assay targets

Integrative genomic biomarkers

MSI, TMB

Genes

The following genes in the panel have full coding sequence coverage for SNV/Indel analysis. Coding sequence was determined using NCBI RefSeq transcripts†. These genes are also enabled for Copy Number Variation (CNV) analysis.

ABL1	*CCND1*	*EIF1AX*	*FLT4*	*KANSL1*	*MST1R*	*PLCB4*	*RPL5*	*TFRC*
ABL2	*CCND2*	*ELF3*	*FOXA1*	*KDM5A*	*MTOR*	*PLCG1*	*RPS6KB1*	*TGFBR1*
ACVR1	*CCND3*	*EP300*	*FOXA2*	*KDM5C*	*MUC16*	*PLXNB2*	*RPTOR*	*TGFBR2*
ACVR2A	*CCNE1*	*EPAS1*	*FOXL2*	*KDM6A*	*MUC6*	*PMS1*	*RRAS2*	*TGIF1*
AKT1	*CD274 (PD-L1)*	*EPCAM*	*FOXO1*	*KDR*	*MUTYH*	*PMS2*	*RUNX1*	*THRAP3*
AKT2	*CD70*	*EPHA2*	*FOXP1*	*KEAP1*	*MYC*	*POLD1*	*RUNX1T1*	*TLR4*
AKT3	*CD79A*	*EPHA3*	*FOXQ1*	*KEL*	*MYCL (MYCL1)*	*POLE*	*RXRA*	*TMSB4X*
ALK	*CD79B*	*EPHA7*	*FUBP1*	*KIF1A*	*MYCN*	*POLQ*	*SCAF4*	*TNFAIP3*
APC	*CDC73*	*EPHB1*	*GATA1*	*KIT**	*MYD88*	*POLRMT*	*SDHA*	*TNFRSF14*
AR	*CDH1*	*ERBB2*	*GATA2*	*KLF4*	*MYH9*	*PPARG*	*SDHB*	*TP53*
ARAF	*CDK12*	*ERBB3*	*GATA3*	*KLF5*	*NBN*	*PPM1D*	*SDHC*	*TP63*
ARHGAP35	*CDK4*	*ERBB4*	*GEN1*	*KMT2A (MLL)*	*NCOR1*	*PPP2R1A*	*SDHD*	*TRAF3*
ARID1A	*CDK6*	*ERCC1*	*GLI1*	*KMT2B*	*NF1*	*PPP2R2A*	*SETBP1*	*TRAF7*
ARID1B	*CDK8*	*ERCC2*	*GNA11*	*KMT2C*	*NF2*	*PPP6C*	*SETD2*	*TSC1*
ARID2	*CDKN1A*	*ERCC4*	*GNA13*	*KMT2D (MLL2)*	*NFE2L2*	*PRDM1*	*SF3B1*	*TSC2*
ARID5B	*CDKN1B*	*ERG*	*GNAQ*	*KRAS*	*NFKBIA*	*PRKAR1A*	*SH2D1A*	*TSHR*
ASXL1	*CDKN2A*	*ERRFI1*	*GNAS*	*KRT222*	*NIPBL*	*PRKD1*	*SLX4*	*TXNIP*
ASXL2	*CDKN2B*	*ESR1*	*GPS2*	*LAMP1*	*NKX2-1*	*PRKDC*	*SMAD2*	*U2AF1*

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*ATM**	*CDKN2C*	*EWSR1*	*GRIN2D*	*LATS1*	*NOTCH1**	*PSIP1*	*SMAD3*	*UNCX*
ATR	*CEBPA*	*EZH2*	*GRM3*	*LATS2*	*NOTCH2*	*PTCH1*	*SMAD4*	*USP9X*
ATRX	*CHD1*	*FAM175A*	*H3F3A*	*LEMD2*	*NOTCH3*	*PTEN*	*SMARCA4*	*VHL*
AURKA	*CHD3*	*FAM46C*	*H3F3B*	*LRP1B*	*NOTCH4*	*PTMA*	*SMARCB1*	*WT1*
AURKB	*CHD4*	*FAM46D*	*H3F3C*	*LZTR1*	*NPM1*	*PTPDC1*	*SMC1A*	*XPO1*
AXIN1	*CHD8*	*FANCA*	*HGF*	*MACF1*	*NRAS*	*PTPN11*	*SMC3*	*XRCC2*
AXIN2	*CHEK1*	*FANCC*	*HIST1H1C*	*MAP2K1 (MEK1)*	*NSD1*	*PTPRC*	*SMO*	*XRCC3*
AXL	*CHEK2**	*FANCD2*	*HIST1H1E*	*MAP2K2 (MEK2)*	*NTRK1*	*PTPRD*	*SOCS1*	*ZBTB20*
B2M	*CIC*	*FANCE*	*HIST1H2BD*	*MAP2K4*	*NTRK2*	*PTPRT*	*SOX17*	*ZFHX3*
BAP1	*COL5A1*	*FANCF*	*HIST1H3B*	*MAP3K1*	*NTRK3*	*RAC1*	*SOX2*	*ZMYM2*
BARD1	*CREBBP*	*FANCG*	*HIST1H3C*	*MAP3K13*	*NUP93*	*RAD21*	*SOX9*	*ZMYM3*
BCL2	*CRKL*	*FANCI*	*HNF1A*	*MAP3K4*	*PALB2*	*RAD50*	*SPEN*	*ZNF750*
BCL2L1	*CSDE1*	*FANCL*	*HOXB13*	*MAPK1*	*PARP1*	*RAD51*	*SPOP*	
BCL2L11	*CSF1R*	*FAT1*	*HRAS*	*MAX*	*PAX5*	*RAD51B*	*SPTA1*	
BCL6	*CSF3R*	*FBXW7*	*HUWE1*	*MCL1*	*PAX8*	*RAD51C*	*SPTAN1*	
BCOR	*CTCF*	*FGF1*	*IDH1*	*MDM2*	*PBRM1*	*RAD51D*	*SRC*	
BCORL1	*CTLA4*	*FGF19*	*IDH2*	*MDM4*	*PDCD1 (PD-1)*	*RAD52*	*SRSF2*	
BIRC3	*CTNNA1*	*FGF2*	*IGF1R*	*MECOM*	*PDCD1LG2 (PD-L2)*	*RAD54L*	*STAG1*	
BLM	*CTNNB1**	*FGF3*	*IKBKE*	*MED12*	*PDGFRA**	*RAF1*	*STAG2*	
BMPR1A	*CUL3*	*FGF4*	*IKZF1*	*MEF2B*	*PDGFRB*	*RARA*	*STAT3*	
*BRAF**	*CYSLTR2*	*FGF7*	*IL6ST*	*MEN1*	*PGR*	*RASA1*	*STK11*	
*BRCA1**	*DAXX*	*FGF8*	*IL7R*	*MET**	*PHF6*	*RB1*	*SUFU*	
*BRCA2**	*DDR2*	*FGF9*	*INPP4B*	*MGA*	*PIK3C2B*	*RBM10*	*SYK*	
BRIP1	*DDX3X*	*FGFR1*	*INPPL1*	*MGMT*	*PIK3C2G*	*RECQL4*	*TAF1*	
BTG1	*DICER1*	*FGFR2*	*IRF2*	*MITF*	*PIK3CA*	*REL*	*TBL1XR1*	
BTG2	*DMD*	*FGFR3*	*IRF4*	*MLH1*	*PIK3CB*	*RET**	*TBX3*	
BTK	*DNMT3A*	*FGFR4*	*IRF6*	*MLLT3*	*PIK3CD*	*RHEB*	*TCEB1*	
CACNA1A	*DOT1L*	*FH*	*IRS2*	*MPL*	*PIK3CG*	*RHOA*	*TCF3*	
CARD11	*EEF1A1*	*FLCN*	*JAK1*	*MRE11A*	*PIK3R1**	*RICTOR*	*TCF7L2*	
CASP8	*EEF2*	*FLNA*	*JAK2*	*MSH2*	*PIK3R2*	*RIT1*	*TERT*	
CBFB	*EGFR*	*FLT1*	*JAK3*	*MSH3*	*PIK3R3*	*RNF43*	*TET1*	

CBL	*EGR3*	*FLT3*	*JUN*	*MSH6*	*PIM1*	*ROS1*	*TET2*

†Contact adx-tech@idtdna.com for the panel target file to view complete list of targeted regions.
*Indicates that select regions of this gene are enabled for Structural Variant analysis in the GTF.

SNPs and sites targeted for sample tracking

rs560681	rs430046	rs987640	rs10776839	rs12393891
rs740598	rs8078417	rs6444724	rs6530357	chrX:4429309
rs1498553	rs9951171	rs6811238	rs5971553	chrX:11314433
rs10773760	rs576261	rs13182883	rs5953060	chrY:6738552
rs1058083	rs1109037	rs214955	rs6524626	chrY:19490214
rs4530059	rs1523537	rs321198	rs5940270	
rs1821380	rs221956	rs4606077	rs722847	

SNPs may be used in combination to uniquely tag and track samples over time. Contact archer-tech@idtdna.com for further details.

Limitations of use

For research use only. Not for use in diagnostic procedures. Unless otherwise agreed to in writing, IDT does not intend these products to be used in clinical applications and does not warrant their fitness or suitability for any clinical diagnostic use. Purchaser is solely responsible for all decisions regarding the use of these products and any associated regulatory or legal obligations.

Safety data sheets pertaining to this product are available upon request.